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SEQUENCE LISTING

<110> Genentech, Inc.  
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Wood, William, I.

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His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
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Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
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Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
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290	295	300	
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&lt;211&gt; 164

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&lt;400&gt; 12

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Glu	Asn	Arg	Gln	Trp	His	Gly	Gly	Ser	Arg	His	Asp	Gln	Ser	His	Gln
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<213> Homo sapiens  
  
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gggggaggcag tgctggaccg cgcgcatccg cgcaagtggc ctccctgaccg tcatacggaa 180  
aggctgcagc ttgaactcgc tggatgaactc acaggactac tacgtggca agaagaacat 240  
cacgtgcgtg gacaccgact ttgtcaacgc cagccccggc catgccctgc agccggctgc 300  
cgccatcatt gcgcgtctcc ctgcactcgg cctgcgtctc tggggaccccg gccagctata 360  
ggctctgggg ggccccgctg cagccccacac tgggtgtgtt gccccaggcc tetgtgccc 420  
tcctcacaga cctggcccaag tggggactctg tcctgggtcc tgaggcacat cctaacgcaa 480  
gtctgaccat gtatgtctgc accccctgtcc cccaccctga ccctcccatg gccctctcca 540  
ggactcccac ccggcagatc agctctagtg acacagatcc gcctgcagat ggcctctcca 600  
accctctctg ctgtgtttc catggcccaag cattctccac ccttaacccct gtgtcagggc 660  
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc caggtctgg 720  
ccgtgggtgtc ccccgaccc agcaggggac aggactcag gagggcccaag taaaggctga 780  
gatgaagtgg actgagtaga actggaggac aagagtgcac gtgagttctt gggagtctcc 840  
agagatgggg cctggaggcc tggaggaagg ggcaggcct cacattcgtg gggctccctg 900  
aatggcagcc tgagcacagc gttaggcctt aataaacacc tgttggataa gccaaaaaaaa 960  
  
<210> 18  
<211> 189  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 18

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Thr	Pro	Thr	Cys	Ala	Thr	Pro	Ala	Gly	Pro	Met	Pro	Cys	Ser	Arg	Leu
				20				25					30		

Pro	Pro	Ser	Leu	Arg	Cys	Ser	Leu	His	Ser	Ala	Cys	Cys	Ser	Gly	Asp
				35				40					45		

Pro	Ala	Ser	Tyr	Arg	Leu	Trp	Gly	Ala	Pro	Leu	Gln	Pro	Thr	Leu	Gly
				50			55				60				

Val	Val	Pro	Gln	Ala	Ser	Val	Pro	Leu	Leu	Thr	Asp	Leu	Ala	Gln	Trp
				65			70			75			80		

Glu	Pro	Val	Leu	Val	Pro	Glu	Ala	His	Pro	Asn	Ala	Ser	Leu	Thr	Met
				85				90					95		

Tyr	Val	Cys	Thr	Pro	Val	Pro	His	Pro	Asp	Pro	Pro	Met	Ala	Leu	Ser
				100				105				110			

Arg	Thr	Pro	Thr	Arg	Gln	Ile	Ser	Ser	Ser	Asp	Thr	Asp	Pro	Pro	Ala
				115			120				125				

Asp	Gly	Pro	Ser	Asn	Pro	Leu	Cys	Cys	Cys	Phe	His	Gly	Pro	Ala	Phe
				130			135			140					

Ser	Thr	Leu	Asn	Pro	Val	Leu	Arg	His	Leu	Phe	Pro	Gln	Glu	Ala	Phe
				145			150			155			160		

Pro	Ala	His	Pro	Ile	Tyr	Asp	Leu	Ser	Gln	Val	Trp	Ser	Val	Val	Ser
				165				170			175				

Pro	Ala	Pro	Ser	Arg	Gly	Gln	Ala	Leu	Arg	Arg	Ala	Gln			
				180				185							

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctcctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20

tgcacaaggc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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 gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180  
 caagcacgtg caggtcaccg gggtcgcat ctccgcccacc gccgaggacg gcaacaagtt 240  
 tgccaagctc atatgtggaga cggacacgtt tggcagccgg gttcgcatca aaggggctga 300  
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 gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg cttccagaa 420  
 cggccggcac gagggtcggt tcatggcctt cacgceggcag gggcggccccc gccaggcttc 480  
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 gcccttcccc aaccaccccg agaaggagaa gcagttcgag ttgtgggct ccgc(cccac 600  
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 gacgggtggc aggcctgga gaggaactga gtgtcaccct gatctcaggc caccagcctc 900  
 tgccggcctc ccagccggc tcctgaagcc cgctgaaagg tcagcgactg aaggcccttgc 960  
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 ccccagcccc caaactcttc ctggctagac tgttaggaagg gacttttgtt tggttgggg 1080  
 tttcaggaaa aaagaaaagg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140  
 acgaccagg cctgcacccccc acccccaact cccagccccc gaataaaacc atttcctgc 1200

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23  
 Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
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Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

<210> 24  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 24  
 cagtagtga gggaccaggcgccatga

<210> 25

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 25
ccgggtaccc gcacgtgctt gcca                                24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<220>
<221> modified_base
<222> (21)
<223> a, t, c or g

<400> 26
gcggatctgc cgcctgctca nctggtcggt catggcgccc t                                41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 27
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ttaccatacg ccctcaggac gttccctcta gctggagtcc tgacttcaa cagaacccca 180
tccatgttgc ttgattttgc ttgtttttttt ttctttttcc caccacattt 240
tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300
ctttttccctt gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
tccctggcctg cccttagtgc tgccgcgtcg acaggaactt tgtctactgt aatgagcgaa 420
gttgcacctc agtgcctttt gggatccccgg agggcgtaac cgtactctac ctccacaaca 480
accaaattaa taatgttgg tttcctgcag aactgcacaa ttttgcgtcg gtgcacacgg 540
tctacactgttgc ttggcaaccaa ctggacgaat tccccatgaa ctttcccaag aatgtcagag 600
ttctccattt gcaggaaaaac aatattcaga ccatttcacg ggctgctt gcccagctct 660
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caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

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 acgtgcgggg ttcatgtgc caaggtcctg aacaagtccg ggggatggcc gtcaggaaat 1320  
 taaatatgaa tctttgtcc tgcacca cgacccccgg cctgcctctc ttcacccca 1380  
 ccccaagtac agcttctccg accactcagc ctcccacccct ctctattcca aacccttagca 1440  
 gaagctacac gcctccaact cctaccacat cgaaacttcc cacgattcct gactggatg 1500  
 gcagagaaag agtgacccca cctattctg aacggatcca gctctctatc cattttgtga 1560  
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 cctcccgagaa gtgaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040  
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 tctttgttt ttaaatctt 2479

<210> 28  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
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 Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
 35 40 45  
 Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
 50 55 60  
 Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
 65 70 75 80  
 Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
 85 90 95  
 Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
 100 105 110  
 Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
 115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val		
420	425	430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met		
435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
640		
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
660		
<210> 29		
<211> 21		
<212> DNA		

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 29
cgggtctacct gtagtggcaac c                                21

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 30
gcaggacaac cagataaaacc ac                                22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 31
acgcagagatt gagaaggctg tc                                22

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 32
ttcacgggct gctcttgccc agctcttcaa gcttgaagag ctgcac    46

<210> 33
<211> 3449
<212> DNA
<213> Homo sapiens

<400> 33
acttggagca agcggcgccg goggagacag aggcagaggc agaagctggg gctccgtcct 60
cgccctccac gagcgttccc cgaggagac cgccggccctc ggcgaggcga agaggccgac 120

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ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatata 3360  
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 ttatacaata ttaaaattca ccacttcag 3449

<210> 34  
 <211> 915  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
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 Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30  
 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45  
 Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60  
 Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80  
 Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95  
 Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110  
 Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125  
 His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140  
 Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160  
 Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175  
 Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190  
 Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205  
 Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220  
 Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245	250	255	
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260	265	270	
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275	280	285	
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290	295	300	
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305	310	315	320
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325	330	335	
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340	345	350	
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355	360	365	
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370	375	380	
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385	390	395	400
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405	410	415	
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420	425	430	
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435	440	445	
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450	455	460	
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470	475	480
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485	490	495	
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500	505	510	

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525

Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540

Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560

Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575

Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590

Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605

Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620

Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640

Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750

Val Gly Lys Ala Ile Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
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 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
                   820                      825                  830  
  
 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
                   835                      840                  845  
  
 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
                   850                      855                  860  
  
 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
                   865                      870                  875                  880  
  
 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
                   885                      890                  895  
  
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 Arg Tyr Arg  
                   915  
  
 <210> 35  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe  
  
 <400> 35  
 gtgaccctgg ttgtgaatac tcc                                  23  
  
 <210> 36  
 <211> 22  
 <212> DNA  
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 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe  
  
 <400> 36  
 acagccatgg tctatacgctt gg                                  22  
  
 <210> 37  
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 <212> DNA  
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35	40	45	
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln			
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
85	90	95	
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
100	105	110	
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
370 375 380

Gln Ala Gly Ser Leu Val  
385 390

<210> 40  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 40  
agggtctcca ggagaaaagac tc

<210> 41  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 41  
atttgtgggcc ttgcagacat agac

<210> 42  
<211> 50  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 42		
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc		50
<210> 43		
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oligonucleotide probe		
<400> 43		
gtgtgacaca gcgtgggc		18
<210> 44		
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<212> DNA		
<213> Artificial Sequence		
<220>		
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oligonucleotide probe		
<400> 44		
gaccggcagg cttctgcg		18
<210> 45		
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oligonucleotide probe		
<400> 45		
cagcagcttc agccaccagg agtgg		25
<210> 46		
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oligonucleotide probe		
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<211> 45  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 47  
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<210> 48  
<211> 2822  
<212> DNA  
<213> Homo sapiens

<400> 48  
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gtgaaatacg caatggaaattt gaagcctgct attgcaacat gggattttca gggaaatggtg 180  
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ctaattgcac taacacagaa ggaagttattt attgtatgtt tgcgttccgc ttcagatcca 300  
gcagtaacca agacagggtt atcaactaatg atggaaaccgt ctgtatagaa aatgtgaatg 360  
caaactgcca tttagataat gtctgtatag ctgc当地atataaact ttaacaaaaaa 420  
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aa 2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

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20 25 30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe  
 35                    40                    45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn  
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly  
65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln  
85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn  
100 105 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys  
115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln  
 130                    135                    140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile  
 145                    150                    155                    160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys  
                   165                  170                  175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480  
 Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
 485 490 495  
 Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510  
 Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
 515 520 525  
 Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
 530 535 540  
 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560  
 Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
 565 570 575  
 Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
 580 585 590  
 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
 595 600 605  
 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
 610 615 620  
 Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
 625 630 635 640  
 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
 645 650 655  
 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
 660 665 670  
 Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
 675 680 685  
 Leu Arg  
 690  
 <210> 50  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> modified\_base  
 <222> (61)

<223> a, t, c or g

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gtatttgtcc ctttgcttc atcatctgac aacttcttat taaaacctca aaatttatgat 180  
aattctgaag aggaggaaag agtcatatct tcagaattt cagtcataat gagctcaaac 240  
ccacccacat tataatgaaact tgaaaaata acaattacat taagtcatcg aaaggtcaca 300  
gataggtata ggagtctatg tggcattttg gaataactcac ctgataccat gaatggcagc 360  
tggtcttcag aggctgtga gctgacatac tcaaattgaga cccacacaccc atgcogctgt 420  
aatcacctga cacatttgc aattttgatg tcctctggc cttccattgg tattaaagat 480  
tataatattt ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540  
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 51  
ggtaatgagc tccattacag 20

<210> 52  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 52  
ggagtagaaaa ggcgcattgg 18

<210> 53  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 53  
cacctgatac catgaatggc ag 22

<210> 54  
<211> 18  
<212> DNA

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 54
cgagctcgaa ttaattcg                                         18

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 55
ggatctcctg agtcagg                                         18

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 56
cctagtttag tgatccttgt aag                                         23

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 57
atgagaccca cacctcatgc cgctgtatac acctgacaca ttttgcatt                                         50

<210> 58
<211> 2137
<212> DNA
<213> Homo sapiens

<400> 58
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cgctaaggcga ggcctcctcc tcccgcagat ccgaacggcc tgggcgggt caccggct 120

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ccatcccaa cggcaactca cagccccgca gcgcattcccg gtgcggccccc agcctccgc 420  
accccccattcg cggagctgc gccgagagcc ccaggaggt gccatgcgg ggggtgtgt 480  
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<210> 59  
<211> 216  
<212> PRT  
<213> *Homo sapiens*

<400> 59  
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
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His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Ile Arg Pro  
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
210 215

<210> 60  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 60  
atccgccccag atggctacaa tgtgtta

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 61  
gcctcccggt ctcctgagc agtgccaaac agcggcagtgt ta



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     35                          40                          45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
     50                          55                          60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
     65                          70                          75                          80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
     85                          90                          95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
     100                          105                          110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
     115                          120                          125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
     130                          135                          140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
     145                          150                          155                          160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
     165                          170                          175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
     180                          185                          190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
     195                          200                          205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
     210                          215                          220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
     225                          230                          235                          240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
     245                          250                          255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
     260                          265                          270  
 Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
     275                          280                          285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
     290                          295                          300  
 Gly Gly Ser Arg Gly Gln Glu Phe

305

310

<210> 65  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 65  
atcggttgtga agtttagtgcc cc

22

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<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 66  
acctgcgata tccaaacagaa ttg

23

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<210> 67
<211> 48
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 67  
ggaaaggaggat acagtcaactc tggaagtatt agtggctcca gcagttcc

48

<210> 68  
<211> 2639  
<212> DNA  
<213> *Homo sapiens*

<400> 68  
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gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata tttacttct 180  
aaataaaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaaagt 240  
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ttggacaatg caattgtggc actggcactt attcagtga agaaaaactt tgtggttcta 360  
tggcattcat catttgacaa atgcaagcat ctcccttatac aatcagctcc tattgaactt 420  
actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480  
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagttac 540

aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttgg 600  
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 taactttccc agccagattt ccagctaaca cacagatttct tctcctacag actaacaata 720  
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 aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcccttctg 840  
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&lt;210&gt; 69

&lt;211&gt; 708

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

Met	Lys	Asp	Met	Pro	Leu	Arg	Ile	His	Val	Leu	Leu	Gly	Leu	Ala	Ile
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Thr	Thr	Leu	Val	Gln	Ala	Val	Asp	Lys	Lys	Val	Asp	Cys	Pro	Arg	Leu
							20		25			30			

Cys	Thr	Cys	Glu	Ile	Arg	Pro	Trp	Phe	Thr	Pro	Arg	Ser	Ile	Tyr	Met
								35		40		45			

Glu	Ala	Ser	Thr	Val	Asp	Cys	Asn	Asp	Leu	Gly	Leu	Leu	Thr	Phe	Pro
								50		55		60			

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
480		
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
560		
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 70  
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ttaccacgt ttttggagta gatgaggaat gggctcgta ttatgtcgac attccagcat 180  
gaatctgtta gacctgttgt taacccgttc cctctccatg tgtctcctcc tacaaggttt 240  
tgttcttatg atactgtgt ttcattctgc cagtagtggtt cccaaGGGCT gtctttgttc 300  
ttccctctggg ggtttaaatg tcacctgttag caatgcAAAT ctcaaggAAA tacctagaga 360  
tcttcctcct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420  
tggaaattttt aaggacctcc atcaacttag agttctcaac ctgtccaaaa atggcattga 480  
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tgacttgtc 540  
cgacaatcggtt attcaaagtgc tgcacaaaaa tgccctcaat aacctgaagg ccaggGCCAG 600  
aattgcAACAC aaccctggc actgcgactg tactctacag caagttctga ggagcatggc 660  
gtccaaatcat gagacagccc acaacgtgtt ctgtaaaacg tccgtgttgg atgaacatgc 720  
tggcagacca ttcctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaaaac 780  
taccgattat gccatgtgg tcaccatgtt tgggtgggtt actatgtga tctcatatgt 840  
ggtatattat gtgaggcaaa atcaggagga tgccccggaga cacctcaat acttgaatc 900  
cctgccaAGC aggccagaaga aagcagatga acctgatgtt attagcactg tggatgtg 960  
tccaaactga ctgtcattga gaaagaaaaga aagtagtttgcgattgcagt agaaataagt 1020  
gttttacttc tcccatccat tgtaaacatt tgaaactttt tatttcgtt tttttgtat 1080  
tatgccactg ctgaactttt aacaaacact acaacataaa taattttgat ttaggtgtc 1140  
cacccttaa ttgtaccccc gatggatat ttctgagtaa gctactatct gaacatttagt 1200  
tagatccatc tcactatatta ataatgaaat ttatTTTTT aatttaaaag caaataaaag 1260  
cttaactttt aaccatgggaa aaaaaaaaaaaa aaaaaaaaaaaa aaaca 1305

<210> 71  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 71

Met	Asn	Leu	Val	Asp	Leu	Trp	Leu	Thr	Arg	Ser	Leu	Ser	Met	Cys	Leu
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Leu	Leu	Gln	Ser	Phe	Val	Leu	Met	Ile	Leu	Cys	Phe	His	Ser	Ala	Ser
					20				25					30	
Met	Cys	Pro	Lys	Gly	Cys	Leu	Cys	Ser	Ser	Ser	Gly	Gly	Leu	Asn	Val
					35			40					45		
Thr	Cys	Ser	Asn	Ala	Asn	Leu	Lys	Glu	Ile	Pro	Arg	Asp	Leu	Pro	Pro
					50			55			60				
Glu	Thr	Val	Leu	Leu	Tyr	Leu	Asp	Ser	Asn	Gln	Ile	Thr	Ser	Ile	Pro
					65			70			75			80	
Asn	Glu	Ile	Phe	Lys	Asp	Leu	His	Gln	Leu	Arg	Val	Leu	Asn	Leu	Ser
					85				90				95		
Lys	Asn	Gly	Ile	Glu	Phe	Ile	Asp	Glu	His	Ala	Phe	Lys	Gly	Val	Ala
					100			105				110			
Glu	Thr	Leu	Gln	Thr	Leu	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Gln	Ser	Val
					115			120			125				
His	Lys	Asn	Ala	Phe	Asn	Asn	Leu	Lys	Ala	Arg	Ala	Arg	Ile	Ala	Asn
					130			135			140				
Asn	Pro	Trp	His	Cys	Asp	Cys	Thr	Leu	Gln	Gln	Val	Leu	Arg	Ser	Met
					145			150			155			160	
Ala	Ser	Asn	His	Glu	Thr	Ala	His	Asn	Val	Ile	Cys	Lys	Thr	Ser	Val
					165				170			175			
Leu	Asp	Glu	His	Ala	Gly	Arg	Pro	Phe	Leu	Asn	Ala	Ala	Asn	Asp	Ala
					180			185			190				
Asp	Leu	Cys	Asn	Leu	Pro	Lys	Lys	Thr	Thr	Asp	Tyr	Ala	Met	Leu	Val
					195			200			205				
Thr	Met	Phe	Gly	Trp	Phe	Thr	Met	Val	Ile	Ser	Tyr	Val	Val	Tyr	Tyr
					210			215			220				
Val	Arg	Gln	Asn	Gln	Glu	Asp	Ala	Arg	Arg	His	Leu	Glu	Tyr	Leu	Lys
					225			230			235			240	
Ser	Leu	Pro	Ser	Arg	Gln	Lys	Lys	Ala	Asp	Glu	Pro	Asp	Asp	Ile	Ser
					245			250			255				
Thr	Val	Val													

&lt;210&gt; 72

&lt;211&gt; 2290

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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 tgctgggctc agtgcgttca ggctcgccca cgggctgccc gcccccgtgc gagtgctccg 180  
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 ccaccgagac ggcgcgtgtc gacctaggca agaaccgcat caaaacgctc aaccaggacg 300  
 agttcgccag ctccccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360  
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 aaaaaaaaaa 2290

&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Val Leu Gly  
     20                        25                        30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
     35                        40                        45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
     50                        55                        60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
     65                        70                        75                        80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
     85                        90                        95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
     100                       105                       110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
     115                       120                       125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
     130                       135                       140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
     145                       150                       155                       160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
     165                       170                       175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
     180                       185                       190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
     195                       200                       205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
     210                       215                       220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
     225                       230                       235                       240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
     245                       250                       255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
     260                       265                       270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
     275                       280                       285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
     290                       295                       300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305                       310                       315                       320  
  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325                       330                       335  
  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340                       345                       350  
  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355                       360                       365  
  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370                       375                       380  
  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385                       390                       395                       400  
  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405                       410                       415  
  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420                       425                       430  
  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435                       440                       445  
  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450                       455                       460  
  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465                       470                       475                       480  
  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485                       490                       495  
  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500                       505                       510  
  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515                       520                       525  
  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530                       535                       540  
  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545                       550                       555                       560  
  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565                       570                       575  
  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
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Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser
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Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile
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<210> 74
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 74
tcacctggag cctttattgg cc                                22

<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 75
ataccagcta taaccaggct gcg                                23

<210> 76
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 76
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      gg                                52

<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

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<400> 77	
ccatgtgtct cctcctacaa ag	22
<210> 78	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 78	
ggaaatagat gtgatctgat tgg	23
<210> 79	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 79	
cacctgttagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg	50
<210> 80	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 80	
agcaaccgcc tgaagctcat cc	22
<210> 81	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 81	
aaggcgcggt gaaagatgt a gacg	24
<210> 82	

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcaactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 agccaggagg cccggccgggaa agcgcgatgg gggcccccagc cgcctcgctc ctgctccctgc 180  
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 agccctggac atctgatgaa acagtggtg gggtggcac cgtggtgctc aagtgc当地 300  
 tgaaaatca cgaggactca tccctgcaat ggtctaaccct tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct ggtaacctt acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagttt acctgtcaa 480  
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<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

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Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
325 330 335

Val Ala Phe Ile Val Phe Leu Leu Ile Met Leu Ile Phe Leu Gly  
340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
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Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
385 390 395

<210> 85  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 85  
gcttaggaatt ccacagaagc cc

<210> 86  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 86  
aacctggaaat gtcaccgagc tg

<210> 87  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

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<400> 87
cctagcacag tgacgaggga cttggc                                26

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 88
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<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 89
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<210> 90
<211> 2755
<212> DNA
<213> Homo sapiens

<400> 90
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn  
20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
                   85                   90                   95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
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 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
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 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
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 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
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 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
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 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
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 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
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 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
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 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp 675	665	670
Cys Gly Ser His Ser Leu Ser Asp 690                               695		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
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22		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
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<210> 94		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
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qtqat						2226

<210> 96  
<211> 490  
<212> PRT  
<213> *Homo sapiens*

<400> 96  
Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
1 5 10 15

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	
<210> 97		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 97		
tggaaggaga tgcgatgcca cctg		24
<210> 98		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 98		
tgaccagtgg ggaaggacag		20

<210> 99		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 99		
acagagcaga gggtgcccttg		20
<210> 100		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 100		
tcagggacaa gtgggtctc tccc		24
<210> 101		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 101		
tcagggagg agtgtgcagt tctg		24
<210> 102		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 102		
acagctcccg atctcagtta ctgcgcgc ggacgaaatc ggcgctcgct		50
<210> 103		
<211> 2026		
<212> DNA		
<213> Homo sapiens		

<400> 103

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tatcccccg ctacctggc cgccccggg cggtgccgc gtgagaggga ggcgcggg 180  
agccgagcgc cggtgtgagc cagcgctgct gccagtgtga gcccgggtg gagcgcgg 240  
ggtgcggagg ggctgtgtg ccggcgcgcg cggctgggg tgaaacccc gagcgtctac 300  
gctgccatga gggcgcgaa cgcctggcg ccactctgcc tgctgtggc tgccgcacc 360  
cagctctcgc ggcagcagtc cccagagaga cctgtttca catgtgtgg cattctact 420  
ggagagtcg gatttattgg cagtgaaggt ttctctggag tgtacccctt aaatagcaa 480  
tgtacttgg aaatcacagt tccccaaggaa aagtagtgc ttctcaattt ccgattata 540  
gacctcgaga gtgacaacct gtgcgcgtat gactttgtgg atgtgtacaa tgccatgcc 600  
aatggccagc gcattggcg cttctgtggc actttccggc ctggagccct tggtccagt 660  
ggcaacaaga tgatggtca gatgattct gatgccaaca cagctgcaaa tggcttcatg 720  
gcccatttcc cgcgtgtga accaaacgaa agaggggatc agtattgtgg aggactcctt 780  
gacagaccc tcggctttaaaaacccca aactggccag accgggatta ccctgcagga 840  
gtcaacttgc tggtgcacat tgtagccccaa aagaatcagc ttatagaatt aaagttttag 900  
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gatgggttta ttgtcacta catattcagg caaaaaaaaac tgcctacaac tacagaacag 1140  
cctgtcacca ccacattccc tgtaaccacg gttttaaaac ccaccgtgc cttgtgtcaa 1200  
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gccccactg ttatcacaac catcactcgc gatgggagtt tgcacccac agtctcgatc 1320  
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gtgttattt tttcaccttc aaggccttgc cctgagggtgt tacaatcttgc tcttgcgttt 1980  
tctaaatcaa tgcttaataa aatattttt aqaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala  
1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr  
20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly  
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr  
 50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr  
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350
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Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro  
           355                     360                     365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu  
           370                     375                     380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys  
           385                     390                     395                 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys  
           405                     410                     415

<210> 105  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 105  
ccgattcata gacctcgaga gt                                 22

<210> 106  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 106  
gtcaaggagt cctccacaat ac                                 22

<210> 107  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 107  
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt                         45

<210> 108  
<211> 1838  
<212> DNA

<213> Homo sapiens

<400> 108

cggacgcgtg	ggccggacgcg	tgggcggccc	acggcgtttcg	cgggctgggg	cggtcgcttc	60
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aagggcctag	tccagctgt	gctctgggc	ctcagcctct	tcctcaacct	cccaggacct	180
atctggctcc	agccctctcc	acctccccag	tcttctcccc	cgccctcagcc	ccatccgtgt	240
catacctgcc	ggggacttgtt	tgacagcttt	aacaaggggc	tggagagaac	catccggac	300
aactttggag	gtgaaaacac	tgcctggag	gaagagaatt	tgtccaaata	caaagacagt	360
gagaccgcgc	tggtagaggt	gctggagggt	gtgtcagca	agtcaactt	cgagtgccac	420
cgcctgtgg	agctgagtga	ggagctgggt	gagagctgg	ggtttcacaa	gcagcaggag	480
gccccggacc	tcttcagtg	gtgtgctca	gattccctga	agctctgtc	ccccgcaggc	540
accttcgggc	cctctgtcct	tccctgtcct	gggggaacag	agaggccctg	cgtggctac	600
gggcagtgtg	aaggagaagg	gacacgaggg	ggcagcgggc	actgtactg	ccaagccggc	660
tacgggggtg	aggcctgtgg	ccagtggtgc	cttggctact	ttgaggcaga	acgcaacgccc	720
agccatctgg	tatgttcggc	ttgttttggc	ccctgtgccc	gatgctcagg	acctgaggaa	780
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gatgagtgtg	gcacagaggg	agccaactgt	ggagctgacc	aattctgcgt	gaacactgag	900
ggctccatcg	agtgcgcgaga	ctgtgcacag	gcctgcctag	gctgcattgg	ggcagggcca	960
ggtcgctgt	agaagtgtag	ccctggctat	cagcagggtgg	gctccaagtg	tctcgatgtg	1020
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ggttatcgct	gcatctgtgc	cgagggctac	aagcagatgg	aaggcatctg	tgtgaaggag	1140
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caggacagct	tggtttattt	ttgagagtgg	ggttaagcacc	cctacctgcc	ttacagagca	1500
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gataccatga	gctttcacc	tggcggggac	tggcaggcgtt	cacaatgtgt	gaatttcaaa	1620
agtttttctt	taatggtggc	tgcttagagct	ttggcccttg	cttaggatta	ggtggccttc	1680
acaggggtgg	ggccatcaca	gctccctctt	gcaagctgca	tgctgcagg	tcctgttctg	1740
tgttacccac	atccccacac	ccattgcca	cttattttatt	catctcagga	aataaaagaaa	1800
ggtcttgaa	agtaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa			1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly  
 1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser  
20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr  
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile  
50 55 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys  
 180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Gly Trp Ala Leu His His  
 225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
355 360 365

Met Phe Phe Gly Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
405 410 415

Ile Lys Gly Arg  
420

<210> 110  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 110  
cctggctatc agcaggtggg ctccaaagtgt ctcgatgtgg atgagtgta 50

<210> 111  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 111  
attctgcgtg aacactgagg gc 22

<210> 112  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 112  
atctgcttgt agccctcgac ac 22

<210> 113



Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190

Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115  
 aggactgccca taacttgcct g 21

<210> 116  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116  
 ataggagttg aagcagcgct gc 22

<210> 117  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117  
 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118  
<211> 1857  
<212> DNA  
<213> Homo sapiens

<400> 118  
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gtcaagtcgtca tcgtgttctt gcctccatcc aagcctacag ttaacatccc ctcccttgcc 480  
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agtgcggcgtt gtgaaggaga attcaaacag acctcgatcat tcctgggtgtg agcctggtcg 960  
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ctctgccttgc tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560  
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accgctgtctc taaagaaaaag aaaactggag gctggggcgc a gttggctcaag cctgtatcc 1680  
cagaggctga ggcaggcggatc tccacctgagg tcggggatcc gggatcagcc tgaccaacat 1740  
ggagaaaaaccct tactggaaat acaaagttag ccaggcatgg tggtgcatgc ctgtgttccc 1800  
agctgcttcag gagcctggca acaagagca aactccagct caaaaaaaaaaaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1                   5                   10                   15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly  
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

<210> 120  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 120  
 tcgcggagct gtgttctgtt tccc

<210> 121  
 <211> 50

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 121		
tgatcgcgat gggcacaaag gcgcaggctc gagaggaaac tgggtgtgcct		50
<210> 122		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 122		
acacctggtt caaagatggg		20
<210> 123		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 123		
taggaagagt tgctgaaggc acgg		24
<210> 124		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 124		
ttgccttact caggtgtac		20
<210> 125		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		

## oligonucleotide probe

<400> 125  
actcagcagt ggttaggaaag 20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
cagcgcgtgg ccggcgccgc tgtgggaca gcatgagcgg cggttggatg ggcagggttg 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgtgtc gtgtctggc ctcggactag 120  
gcctggggc cgccgcgac ccgcgttcca ccccgcaccc tgcccaggcc gcaggcccc 180  
gtcaggctc gtcccaccc accaagttcc agtgcgcac cagtggctta tgcgtcccc 240  
tcacctggcg ctgcgacagg gacttggact gcagegatgg cagcgtatgg gaggagtca 300  
ggattgagcc atgtacccag aaagggcaat gcccacccgc ccctggcctc ccctggccct 360  
gcacccggcgt cagtgtactgc tctggggaa ctgacaagaa actgcgcac ac 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgctgcga cggccacccca gactgtcccg actccagcga cgagctggc tggaaaccca 540  
atgagatcc cccggaaagg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600  
tcacctctct caggaatgcc acaaccatgg ggcccccgt gaccctggag agtgcctcc 660  
ctgtcgaa tgccacatcc tcctctgccc gagaccagtc tggaaaccca actgcctatg 720  
ggtttattgc agtgcgtcg gtgctcgtg caagcctggt caccgcaccc ctcctccctt 780  
tgtcctggct ccgagcccgag gagcgcctcc gcccactggg gtactgggt gccatgaagg 840  
agtccctgtc gctgtcgaa cagaagaccc cgctgcctg aggacaagca cttggccacca 900  
ccgtcactca gcccctggcg tagccggaca ggaggagagc agtgcgtcg atgggtaccc 960  
gggcacacca gcccctcgag acctgagttc ttctggccac gtggaaaccc tcacccgagc 1020  
tcctgcagaa gtggccctgg agattgggg tccctggaca ctcctatgg agatccgggg 1080  
agctaggatg gggAACCTGC cacagccaga actgaggggc tggcccccagg cagctcccg 1140  
gggttagaac gcccctgtgc ttaagacact ccctgtgcc ccgtctgagg gtggcgatttta 1200  
aagttgttc 1210

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                   85                     90                     95  
  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                   100                    105                    110  
  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                   115                    120                    125  
  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                   130                    135                    140  
  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                   145                    150                    155                    160  
  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                   165                    170                    175  
  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                   180                    185                    190  
  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                   195                    200                    205  
  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                   210                    215                    220  
  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
                   225                    230                    235                    240  
  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                   245                    250                    255  
  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                   260                    265                    270  
  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                   275                    280  
  
 <210> 128  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide probe  
  
 <400> 128  
 aagttccagt gccgcaccag tggc  
  
 <210> 129

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 129
ttggttccac agccgagctc gtcg                                24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc      50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cggctctcgct cgctcgcgca gcggcgccag cagaggtcgc gcacagatgc 60
gggttagact ggcgggggga ggaggcgag gagggaaagga agctgcattgc atgagaccca 120
cagactcttg caagctggat gcctctgtg gatgaaaat gtatcatgga atgaacccga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcgat tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg ctccggccct gcacagctca 300
cggcggtt cgatgaccc ttcaaggatgtt ctgaccccgat cattcccgag aatggcttca 360
ggaccccccag cggagggtt ttctttaaag gctctgttagc ccgatttccat tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tggatgttgc gatattttat ggaaccttag 480
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgcccgtatc cctcaaatcg 540
aagatgctga gattcataaac aagacatata gacatggaga gaagctataatc atcaacttgtc 600
atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgctcgatg 660
atgaaacgtt gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatcttctt gagctccaga cctccttccc ggtggggact gtatcttc 780
atcgctgtttt tcccggtt aaacttgcgtt ggtctgcgtt tcttgcgttgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctggat agcccaagtc tgtccactac 900
ctccaaatggt gagtcacggat gatttcgtt gccaccccgat gccttgcgttgc cgctacaacc 960
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acatcacctg ccagtatggat gaggatggatcc tttttatca agtctactgc atcaaatcg 1080
agcaaaacgtt gcccagcacc catgagacccc tcctgaccac gtggaaagatt gtggcggttca 1140

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cggcaaccag tgtgtgtctg gtgtgtgtgc tcgtcatcct gccaggatg ttccagacca 1200  
 agttcaaggc ccacttccc cccaggggc ctccccggag ttccagcagt gaccctgact 1260  
 ttgtggtgt agacggcgtg cccgtcatgc tcccgctcta tgacgaagct gtgagtgccg 1320  
 gcttgagtgc ctttagcccc gggtacatgg cctctgtggg ccaggcgtgc cccttacccg 1380  
 tggacgacca gagcccccca gcataccccc gtcagggga cacggacaca ggcccagggg 1440  
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500  
 ctcccaggtg ccaagagagc acccaccctg ctteggacaa ccctgacata attgccagca 1560  
 cggcagagga ggtggcatcc accagccca gcatccatca tggccactgg gtgttgc 1620  
 taagaaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt ctttccttc tcttggttt agacaaatgt aaacaaagct 1740  
 ctgatcctta aaattgttat gctgatagag tggtgaggc tggaaagctt atcaagtcct 1800  
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1				5				10					15		

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
					20			25				30		

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
				35				40				45			

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
					50			55			60				

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
					65				70		75		80		

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
					85				90			95			

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
					100				105			110			

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
					115				120			125			

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
					130			135			140				

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
						145		150			155			160	

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
					165				170			175			

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
485 490

<210> 133  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 133  
atctcctatc gctgcttcc cg 23

<210> 134  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 134  
agccaggatc gcagtaaaac tcc 23

<210> 135  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 135  
atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136  
<211> 1815  
<212> DNA  
<213> Homo sapiens

<400> 136  
ccccacgcgtc cgctccgcgc cctccccccc gcctcccggtg cggtcgcgtcg gtggcctaga 60  
gtatgtgtcg cccgggttgc agttgtcgcg cacccctctg cccggccagcc cgctccaccc 120  
ccgttagcgcgc cgagtgtcg ggggcgcaacc cgagtcgggc catgaggcccg ggaaccgcgc 180  
tacaggccgt gctgtgtggc gtgtgtgtgg tggggctgctg ggcggcgacg ggttcgcctgc 240  
tgatgtgcctc ggatttggac ctcaqaggag qgcagccagt ctgccccggga qggacacaga 300

ggccttgta	taaagtcat	tactccatg	atacttcgt	aagactgaac	ttttaggaag	360
ccaaaagaac	ctgcaggagg	gatggaggcc	agctagtctg	catcgagtct	gaagatgaac	420
agaaaactgt	agaaaagttc	attgaaaacc	tcttgcatt	tgatggatgc	ttctggattt	480
ggctcaggag	gcgtgaggag	aaacaagca	atagcacagc	ctgccaggac	ctttatgttt	540
ggactgtatgg	cagcatatca	caatttagga	actggatgt	ggatgagccg	tcctcgccca	600
gcgaggctgt	cgtggtcatt	taccatcagc	catcgccacc	cgtggccatc	ggaggcccct	660
acatgttcca	gtggaatgtat	gaccggtgca	acatgaagaa	caatttcatt	tgc当地atatt	720
ctgatgagaa	accaggcgtt	cctttagag	aagctgaagg	tgagaaaca	gagctgacaa	780
cacctgtact	tccagaagaa	acacaggaaag	aagatgc当地	aaaaacattt	aaagaaaagta	840
gagaagctgc	cttgaatctg	gcctacatcc	taatccccag	cattccctt	ctc当地ctcc	900
tttgtggcac	cacagttgtt	tgttgggtt	ggatctgtat	aaaaagaaaa	cgggagcagc	960
cagaccctag	cacaaagaag	caacacacca	tctggccctc	tcctcaccag	ggaaacagcc	1020
cgAACCTAGA	GGTCTACAAAT	GTCATAAGAA	AACAAAGCAG	AGCTGACTTA	GCTGAGACCC	1080
ggccagacct	gaagaatatt	tcattccgag	tgttgggg	agaaggccact	cccgatgaca	1140
tgtcttgta	ctatgacaac	atggctgtat	accatcaga	aagtgggtt	gtgactctgg	1200
tgagcgttga	gagtggattt	gtgaccaatg	acatttatga	gttctccca	gaccaaattgg	1260
ggaggagtaa	ggagtcttgg	tgggtggaaa	atgaaatata	tggttattag	gacatataaa	1320
aaactgaaaac	tgacaacaat	ggaaaagaaa	tgataagcaa	aatccttta	ttttctataa	1380
ggaaaatatac	cagaaggct	atgaacaagc	ttagatcagg	tcctgtggat	gagcatgtgg	1440
tccccacgac	ctctgttgg	accccccacgt	tttggctgtat	tcctttatcc	cagccagtca	1500
tccagctcga	ccttatgaga	aggtacccgt	cccaggctgt	gcacatagta	gagtctcaat	1560
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atattatcat	acagacagaa	aatccagaat	cttttcaaag	cccacatatg	gtgc当地cagg	1740
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agcaggaaaa	aaaaaa					1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
                  35                 40                 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
           100                 105                 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

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<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 138
gttcattgaa aacctttgc catctgatgg tgacttctgg attgggctca      50

<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 139
aagccaaaga agcctgcagg aggg      24

<210> 140
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 140
cagtccaagc ataaaggta tggc      24

<210> 141
<211> 1514
<212> DNA
<213> Homo sapiens

<400> 141
ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
gcatccgcag gttcccgccg acttgggggc gcccgcgtgag ccccgccgcgc cgccagaagac 120
tttgtttgc ctcctgcagc ctcaaccggg agggcagcga ggcctacca ccatgatcac 180
tggtgtgttc agcatgcgt tgggacccc agtgggcgtc ctgacactgc tggcgtactg 240
cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc agtgtccgg 300
cgaccgcagc ctgtcaagt taaaaatggt gcaggtcggt ttgcacacg gggctcggag 360
tcctctcaag ccgtccccgc tggaggagca ggttagagtgg aaccccccacg tattagaggt 420
cccaccccaa actcagttt attacacagt caccaatcta gctgggtggtc cgaaaccata 480
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gctgaccaag gtgggcgtgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600
tgtgaaagac attcccttgc ttccaccaac cttcaacccca caggaggctt ttattcggtc 660
cactaacatt ttccggaaatc tggagtccac ccgttgtttgc ctggctgggc tttccagtg 720

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tcagaaaagaa ggaccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780  
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 ttacagcca ggaatctcg aggattgaa aaaggtaag gacaggatgg gcattgacag 900  
 tagtgataaa gtggacttct tcatccctcg ggacaacgtg gctgccgagc aggcacacaa 960  
 cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020  
 cacatccttg tacatactgc ccaaggaaga cagggaaagt ctccagatgg cagtaggccc 1080  
 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccca 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctctaata 1200  
 gaccctgggg attttgacc acaaatggcc accgttgct gtgacctga ccatggaact 1260  
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 ggtgccgaga ggttgcctg atggctcg cccgctggac atgttcttga atgccatgtc 1380  
 agtttataacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440  
 agttggaaat gaagagtaac tgatttataa aagcaggatg tttgatattt aaaataaaat 1500  
 gccttataac aatg 1514

&lt;210&gt; 142

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met	Ile	Thr	Gly	Val	Phe	Ser	Met	Arg	Leu	Trp	Thr	Pro	Val	Gly	Val
1							5				10				15

Leu	Thr	Ser	Leu	Ala	Tyr	Cys	Leu	His	Gln	Arg	Arg	Val	Ala	Leu	Ala
								20				25			30

Glu	Leu	Gln	Glu	Ala	Asp	Gly	Gln	Cys	Pro	Val	Asp	Arg	Ser	Leu	Leu
							35			40			45		

Lys	Leu	Lys	Met	Val	Gln	Val	Val	Phe	Arg	His	Gly	Ala	Arg	Ser	Pro
			50					55				60			

Leu	Lys	Pro	Leu	Pro	Leu	Glu	Glu	Gln	Val	Glu	Trp	Asn	Pro	Gln	Leu
							65			70		75			80

Leu	Glu	Val	Pro	Pro	Gln	Thr	Gln	Phe	Asp	Tyr	Thr	Val	Thr	Asn	Leu
						85				90			95		

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu
							100			105			110		

Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly
						115					120		125		

Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val
			130					135				140			

Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe
			145						150			155			160

Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu
								165			170			175	

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
                  180                             185                         190  
  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
                  195                         200                         205  
  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
                  210                         215                         220  
  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
                  225                         230                         235                 240  
  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
                  245                         250                         255  
  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
                  260                         265                         270  
  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
                  275                         280                         285  
  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
                  290                         295                         300  
  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
                  305                         310                         315                 320  
  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
                  325                         330                         335  
  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
                  340                         345                         350  
  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
                  355                         360                         365  
  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
                  370                         375                         380  
  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
                  385                         390                         395                 400  
  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
                  405                         410                         415  
  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
                  420                         425  
  
 <210> 143  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 143
ccaaactacca aagctgctgg agcc                                24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 144
gcagctctat taccacggga agga                                24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 145
tccttcccgt ggtaatagag ctgc                                24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg      45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
cttaaatttc agctcatcac cttcacctgc cttggtcatg gctctgctat tctccttgat 120
ccttgcatt tgcaccagac ctggattcct agcgcttcca tctggagtgc ggctgggtggg 180

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gggcctccac	cgttgtgaag	ggcggttgg	ggttggAACAG	aaaggccagt	ggggcaccgt	240
gtgtgatgac	ggctggaca	ttaaggacgt	ggctgtgtt	tgccgggagc	tggctgtgg	300
agctgccagc	gaaacccta	gtggtatttt	gtatgagcca	ccagcagaaa	aagagaaaa	360
ggtcctcatc	caatcagtca	gttgcacagg	aacagaagat	acattggctc	agtgtgagca	420
agaagaagtt	tatgattgtt	cacatgtat	agatgctgg	gcatcggtg	agaacccaga	480
gagcttttc	tccccagtc	cagagggtgt	caggctggct	gacggccctg	ggcattgca	540
gggacgcgtg	gaagtgaagc	accagaacca	gtggtatacc	gtgtgccaga	caggctggag	600
cctccgggcc	gcaaagggtgg	tgtgccgca	gctggatgt	gggagggtgt	tactgactca	660
aaaacgcgtc	aacaaggcatg	cctatggccg	aaaacccatc	tggctgagcc	agatgtcatg	720
ctcaggacga	gaagcaaccc	ttcaggattt	cccttctggg	ccttggggga	agaacacctg	780
caaccatgt	gaagacacgt	gggtcgaat	tgaagatccc	tttgacttga	gacttagg	840
aggagacaa	ctctgtctg	ggcacttgg	ggtgtctgcac	aagggttat	gggtctgt	900
ctgtgatgac	aactggggag	aaaaggagga	ccaggtggta	tgcaagcaac	tggctgtgg	960
gaagtccctc	tctccctct	tcagagaccg	gaaatgttat	ggccctgggg	ttggccgcat	1020
ctggctggat	aatgttctt	gctcaggga	ggagcagtcc	ctggagcagt	gccagcacag	1080
attttgggg	ttcacgact	gcacccacca	ggaagatgt	gctgtcatct	gctcaagtgt	1140
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atttactgtc	tacatgactg	catggatga	acactgtat	tcttctgccc	ttggactggg	1260
acttataactt	ggtccccctg	attctcaggc	cttcagagtt	ggatcagaac	ttacaacatc	1320
aggcttagtt	ctcaggccat	cagacatagt	tttggactac	atcaccacct	ttccatatgtc	1380
tccacattgc	acacagcaga	ttcccagct	ccataattgt	gtgtatcaac	tacttaaata	1440
cattctcaca	cacacacaca	cacacacaca	cacacacaca	cacacataca	ccatttgc	1500
tgtttctctg	aagaactctg	acaaaataca	gattttggta	ctgaaagaga	ttctagagga	1560
acggaatttt	aaggataaat	tttctgaatt	ggttatgggg	tttctgaaat	tggctctata	1620
atctaattag	atataaaatt	ctggtaactt	tatttacaat	aataaaagata	gcactatgtg	1680
ttcaaa						1686

<210> 148  
<211> 347  
<212> PRT  
<213> *Homo sapiens*

<400> 148  
Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
 35                    40                    45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 149	
ttcagctcat caccttcacc tgcc	24
<210> 150	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 150	
ggctcataca aaataccact aggg	24
<210> 151	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 151	
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt	50
<210> 152	
<211> 1427	
<212> DNA	
<213> Homo sapiens	
<400> 152	
actgcactcg gttctatcg ttgaattccc cggggatcct cttagagatcc ctgcaccccg 60	
acccacgcgt ccgcggacgc gtgggcggac gcgtggccg gctaccagga agagtctgcc 120	
gaaggtgaag gccatggact tcatcaccc cacagccatc ctgcacctgc tgttcggctg 180	
cctggcgctc ttccggctct tcggctgct gcagtgggtg cgcggaaagg cctacctgcg 240	
aatgtctgtg gtggtgatca caggcgccac ctcagggctg gcaaaagaat gtgcaaaagt 300	
cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360	
gctcatcaga gaacttaccg ctctcatgc caccaagggt cagacacacaca agccttactt 420	
ggtgacccctc gacccacag actctggggc catagttgca gcagcagctg agatcctgca 480	
gtgctttggc tatgtcgaca tacttgtcaa caatgtggg atcagctacc gtggtaccat 540	
catggacacc acagtggatg tgacaagag ggtcatggag acaaactact ttggcccaagt 600	
tgtcttaacg aaagcactcc tgcctccat gatcaagagg aggcaaggcc acattgtcgc 660	
catcagcgc atccaggggca agatgagcat tcctttcga tcagcatatg cagccctccaa 720	
gcacgcaacc caggcttct ttgactgtct gcgtggcgag atgaaacagt atgaaattga 780	
ggtgaccgtc atcagccccg gtcacatcca caccaaccc tctgtaaaatg ccatcaccgc 840	
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gcccctgtgga 900	
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catggcctcc agggccagaa aagagcggaa atccaagaac tcctagact ctgaccagcc 1080	

agggccaggc cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140  
 ttgttgagac tttatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200  
 gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttccttc cagggtgagg 1260  
 gaaaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320  
 tctcaaacag taaaaaaaaaaa aaaaaaggc ggccgcgact ctagagtcga cctgcagaag 1380  
 ctggccgcc atggcccaac ttgtttattt cagttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met	Asp	Phe	Ile	Thr	Ser	Thr	Ala	Ile	Leu	Pro	Leu	Leu	Phe	Gly	Cys
1															15

Leu	Gly	Val	Phe	Gly	Leu	Phe	Arg	Leu	Leu	Gln	Trp	Val	Arg	Gly	Lys
															30
20															
25															

Ala	Tyr	Leu	Arg	Asn	Ala	Val	Val	Val	Ile	Thr	Gly	Ala	Thr	Ser	Gly
35															45

Leu	Gly	Lys	Glu	Cys	Ala	Lys	Val	Phe	Tyr	Ala	Ala	Gly	Ala	Lys	Leu
50															60

Val	Leu	Cys	Gly	Arg	Asn	Gly	Gly	Ala	Leu	Glu	Glu	Leu	Ile	Arg	Glu
65															80

Leu	Thr	Ala	Ser	His	Ala	Thr	Lys	Val	Gln	Thr	His	Lys	Pro	Tyr	Leu
85															95

Val	Thr	Phe	Asp	Leu	Thr	Asp	Ser	Gly	Ala	Ile	Val	Ala	Ala	Ala	
100															110

Glu	Ile	Leu	Gln	Cys	Phe	Gly	Tyr	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala
115															125

Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Ile	Met	Asp	Thr	Thr	Val	Asp	Val	Asp
130															140

Lys	Arg	Val	Met	Glu	Thr	Asn	Tyr	Phe	Gly	Pro	Val	Ala	Leu	Thr	Lys
145															160

Ala	Leu	Leu	Pro	Ser	Met	Ile	Lys	Arg	Arg	Gln	Gly	His	Ile	Val	Ala
165															175

Ile	Ser	Ser	Ile	Gln	Gly	Lys	Met	Ser	Ile	Pro	Phe	Arg	Ser	Ala	Tyr
180															190

Ala	Ala	Ser	Lys	His	Ala	Thr	Gln	Ala	Phe	Phe	Asp	Cys	Leu	Arg	Ala
195															205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val		
260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
305	310	

<210> 154  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 154  
ggtgctaac tggtgctctg tggc 24

<210> 155  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 155  
cagggcaaga tgagcattcc 20

<210> 156  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 156  
 tcatactgtt ccatctcgcc acgc

24

<210> 157  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 157  
 aatggtgtggg ccctagaaga gtcatacaga gaactcaccg cttctcatgc

50

<210> 158  
 <211> 1771  
 <212> DNA  
 <213> Homo sapiens

<400> 158  
 cccacgcgtc cgctgggttt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
 aaaaaaaaaaa acacaccaaa cgctcgacgc cacaaggatggg atgaaatttc ttctggacat 120  
 cctcctgttt ctcccgttac tgatcgcttg ctcccttagag tccttcgtga agcttttat 180  
 tcctaagagg agaaaatcg tcacccggcga aatcgctgtt attacaggag ctggcatgg 240  
 aattgggaga ctgactgcct atgaatttgc taaaactttaaa agcaagctgg ttctctggga 300  
 tataaataag catggactgg agggaaacacgc tgccaaatgc aaggactgg gtgccaaggt 360  
 tcataccctt gtggtagact gcagcaacccg agaagatatt tacagcttg ccaaagaaggt 420  
 gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggttag tctatacatc 480  
 agattttgtt gctacacaag atcctcagat tgaaaagact tttgaagttt atgtacttgc 540  
 acattttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatcat 600  
 tggactgtg gcttcggcag ctggacatgt ctggcccccc ttcttactgg cttactgttc 660  
 aagcaagttt gctgtgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
 aataacttgg a gtcaaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780  
 aaatccaagt acaagttgg gacccactct ggaaccttag gaaatgttac 840  
 gcatgggatt ctgactgagc agaagatgtat ttttattcca tttttatagat ctttttaac 900  
 aacatttggaa aggatccctt ctgagcggtt cctggcagtt taaaacacaa aaatcgtgt 960  
 taagtttgcgtt gcaatttttgc gatataaaat gaaagcgcac taagcaccta gtttctgaa 1020  
 aactgtatccat ccagggttttgc gttgatgtca tctaatacgat ccagaattttt aatgtttgaa 1080  
 cttctgtttt ttcttaattt ccccttttgc tcaatatcat ttttgaggct ttggcagtt 1140  
 tcattttacta ccacttggc ttttagccaaa agctgattac atatgatata aacagagaaaa 1200  
 tacctttaga ggtgacttta agggaaatga agaaaaagaa cccaaatgac tttttaaaaa 1260  
 taatttccaa gattattttgt ggctcacctg aaggcttgc aaaatttgc ccataaccgt 1320  
 ttatattaaca tatattttta ttttgatttgc cacttaattt ttgtataatt tttttttttt 1380  
 tttctgtttt acataaaatc agaaaacttca agctctctaa ataaaatgaa ggactatatc 1440  
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 gccactctgtt ttccgttgcgat atacctcaca ttccaaatgcc aaacatttct gcacaggaa 1560  
 gcttagaggtt gatacacgtt ttgcaagtttgcgat aaaagcatca ctgggatttgcggaggaa 1620  
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 aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1740  
 aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1771

<210> 159

<211> 300  
<212> PRT  
<213> *Homo sapiens*

<400> 159  
 Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Pro Leu Leu Ile Val  
 1 5 10 15  
  
 Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
 20 25 30  
  
 Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
 35 40 45  
  
 Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
 50 55 60  
  
 Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
 65 70 75 80  
  
 Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
 85 90 95  
  
 Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
 100 105 110  
  
 Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
 115 120 125  
  
 Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
 130 135 140  
  
 Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr  
 145 150 155 160  
  
 Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
 165 170 175  
  
 Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
 180 185 190  
  
 Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
 195 200 205  
  
 Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
 210 215 220  
  
 Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
 225 230 235 240  
  
 Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
 245 250 255

```

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
260           265           270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
275           280           285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290           295           300

<210> 160
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 160
ggtgaaggca gaaatggag atg                                23

<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 161
atccccatgca tcagcctgtt tacc                                24

<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 162
gctgggttag tctatacatc agatttgtt gctacacaag atcctcag      48

<210> 163
<211> 2076
<212> DNA
<213> Homo sapiens

<400> 163
cccacgcgtc cgccggacgcg tgggtcgact agttctagat cgccgagcggc 60
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 attgaagctg ggaagatcca aaaaggaaga gaatttagtt tggcggccc tttcccagga 300  
 ctgaacatga agagttatgc cggttcctc accgtaaata agacttacaa cagcaacctc 360  
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 cagggtggc cggtggatcc atccatgttt ggactcttg tggaaacatgg gccttatgtt 480  
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<210> 164  
 <211> 476  
 <212> PRT  
 <213> Homo sapiens

<400> 164  
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Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln			
85		90	95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100		105	110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115	120		125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130	135		140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145	150	155	160
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165		170	175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180		185	190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195	200		205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210	215		220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225	230	235	240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245		250	255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260		265	270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275		280	285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290	295		300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305	310	315	320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325		330	335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340		345	350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
 355                    360                    365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370                    375                    380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385                    390                    395                    400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405                    410                    415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420                    425                    430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His  
 435                    440                    445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
 450                    455                    460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465                    470                    475

<210> 165  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165  
ttccatgcca cctaaggag actc

24

<210> 166  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166  
tggatgaggt gtgcaatggc tggc

24

<210> 167  
<211> 24  
<212> DNA  
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 167
agctctcaga ggctggcat aggg 24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gtttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
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tatagcataa aggttagaga cccaaaataga taacaggatt ccctgaacat tcctaagagg 600
gagaaaatgtt gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
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<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr

1

2  
5

10

15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly  
 20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
50 55 60

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
 115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val  
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser  
165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450                    455                    460  
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
465                    470                    475                    480  
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
485                    490                    495  
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
500                    505                    510  
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
515                    520                    525  
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
530                    535                    540  
Leu Tyr Phe Leu Gly Glu Gln Arg  
545                    550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaaataccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<400> 173
ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42

<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1683)
<223> a, t, c or g

<400> 174
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tgctggctgt ctgggcttc ctgggtctcc gcaggctgga ctggagcacc ctggccctc 180
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

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Ser	Thr	Leu	Val	Pro	Leu	Arg	Leu	Arg	His	Arg	Gln	Leu	Gly	Leu	Gln
					35				40			45			

Ala	Lys	Gly	Trp	Asn	Phe	Met	Leu	Glu	Asp	Ser	Thr	Phe	Trp	Ile	Phe
					50		55				60				

Gly	Gly	Ser	Ile	His	Tyr	Phe	Arg	Val	Pro	Arg	Glu	Tyr	Trp	Arg	Asp
					65			70			75			80	

Arg	Leu	Leu	Lys	Met	Lys	Ala	Cys	Gly	Leu	Asn	Thr	Leu	Thr	Thr	Tyr
					85				90				95		

Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser
					100			105			110				

Gly	Asn	Leu	Asp	Leu	Glu	Ala	Phe	Val	Leu	Met	Ala	Ala	Glu	Ile	Gly
					115			120				125			

Leu	Trp	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ser	Glu	Met	Asp
					130			135			140				

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 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
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 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
 435                          440                          445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450                          455                          460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
 465                          470                          475                          480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485                          490                          495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500                          505                          510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
 515                          520                          525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
 530                          535                          540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
 545                          550                          555                          560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
 565                          570                          575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
 580                          585                          590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
 595                          600                          605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
 610                          615                          620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
 625                          630                          635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctagggtga ggggtggacg ggtcccagga 60  
 ccctggtagag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120  
 aaggggagca aagccggct cggcccgagg cccccaggac ctccatctcc caatgttgg 180  
 ggaatccgac acgtgacggt ctgtccgccc tctcagacta gaggagcgct gtaaacgcca 240  
 tggtctccaa gaagctgtcc tgccctcggt ccctgctgct gccgctcagc ctgacgctac 300  
 tgctgccccca ggcagacact cggtcggtcg tagtgatag gggcatgac cggttctcc 360  
 tagacggggc cccgtccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgctttgggc cgaccggc ttgaagatgc gatggagogg cctcaacgcc atacagttt 480  
 atgtgccctg gaactaccac gagccacagc ctggggctta taactttat ggcagccgg 540  
 acctcattgc ctttctgaat gaggcagctc tagcAACCT gtggcata ctgagaccag 600  
 gacccttacat ctgtcAGAG tgggagatgg ggggtctccc atcctggtt cttcgaaaac 660  
 ctgaaattca tctaagaacc tcagatccag acttccttc cgcAGTGGAC tcctggttca 720  
 aggtcttgct gcccaagata tatccatggc tttatcacaa tggggcaac atcattagca 780  
 ttcaggtgga gaatgaatat ggtagctaca gaggcgttga cttcagctac atgaggcact 840  
 tggctggcctt cttccgttca ctgtcAGAG aaaagatctt gctttcacc acagatggc 900  
 ctgaaggact caagtgtgc tccctccggg gactctatac cactgttagat tttggccag 960  
 ctgacaacat gaccaaaatc ttacccttc ttcggaaagta tgaaccccat gggccattgg 1020  
 taaaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacgg 1080  
 ctgtgtcAGAG tggtaacccaa ggactagaga acatgtcAA gttgggagcc agtgtgaaca 1140  
 tgtacatgtt ccatggaggt accaactttg gatattggaa tggcgttgc tttggccag 1200  
 gcttccttcc gattactacc agctatgact atgatgcacc tatactgaa gcaggggacc 1260  
 ccacacctaa gcttttgc cttcggatgt tcatcAGAA gttccaggaa gttccttgg 1320  
 gacctttacc tccccccggc cccaagatga tgcttggacc tggactctg cacctgggt 1380  
 ggcattttact ggcttccta gacttgctt gccccctgg gcccattcat tcaatcttc 1440  
 caatgacctt tgaggctgtc aaggcaggacc atggcttcat tggcgttgc acctatatga 1500  
 cccataccat ttttggcca acaccattct gggtgcAAA taatggagtc catgaccgt 1560  
 cctatgtgat ggtggatggg gtgttccagg gtgttgcgg gggaaatatg agagacaaac 1620  
 tatttttgac ggggaaactg ggttccaaac tggatatctt ggtggagaac atggggaggc 1680  
 tcagcttgg gtctaacacgc agtgacttca agggcttgc tggcgttgc acctatatga 1740  
 aaacaatctt tacccgtgg atgatgttcc ctctgaaaat tgataacctt gtgaagtgg 1800  
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 agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160  
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 ggtggctcat gctgttatac ccagcacttt gggaggctga gacgggtggaa ttacctgggg 2280  
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 ggagaattgc ttgaatccag gaggcagagg ttgcgttgc tggaggttgc accactgcac 2460  
 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaaa 2505

<210> 177  
 <211> 654  
 <212> PRT  
 <213> Homo sapiens

<400> 177  
 Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
 1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 179

tggacacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 180

gggcattcacc gaaggagtgg acctttatgg tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

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<210> 182
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 182
tggcacccag aatggtgttg gctc                                         24

<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 183
cgagatgtca tcagcaagtt ccaggaagtt cctttggac ctttacacctc          50

<210> 184
<211> 1947
<212> DNA
<213> Homo sapiens

<400> 184
gcttgaaca cgtctgcaag cccaaagttt agcatcttat tggttatgag gtatttgagt 60
gcacccacaa tatggcttac atgttggaaa agcttctcat cagttacata tccatttattt 120
gtgtttatgg ctttatctgc ctctacactc tcttctggtt attcaggata cctttgaagg 180
aatattcttt cgaaaaaagtc agagaagaga gcagtttag tgacattcca gatgtcaaaa 240
acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagggtt 300
ttggtgtgtt cttgtcagaa gttagtggaaa ataaacttag ggaaatttagt ttgaaccatg 360
agtggacatt tgaaaaactc aggccgcaca tttcacgcaa cgcccaggac aagcaggagt 420
tgcacatgtt catgtgtcg ggggtgccccg atgctgtctt tgacctcaca gacctggatg 480
tgctaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
acctccaaga gctccacccctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600
ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660
cctgggtgta tttgtctaaa aacccatcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
acgtgaagag caatttgacc aaagtccctt ccaacattac agatgtggct ccacatctta 840
caaagtttagt cattcataat gacggcacta aactcttggt actgaacagc cttaagaaaa 900
tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
ttttcagcct ctctaattta caggaactgg atttaaagtcaataacatt cgcacaattt 1020
aggaaatcat cagttccag cattaaaac gactgacttg tttaaaatta tggcataaca 1080
aaattgttac tattcctccc tctattaccc atgtcaaaaaa cttggagtc ctttatttct 1140
ctaacacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcagatgct 1200
tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattt cttcagaacc 1260
tgcagcattt gcatatcact gggAACAAAG tggacattct gccAAACAAAG ttgtttaaat 1320

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gcataaaagt gaggacttg aatctgggac agaactgcat cacctcaactc ccagagaaaag 1380  
 ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttgc 1440  
 cagcccgact gggccagttgt cgatgtca agaaaagcgg gtttgttgta gaagatcacc 1500  
 ttttgatac cctgcccactc gaagtcaaag aggcatggaa tcaagacata aatattccct 1560  
 ttgcaaatgg gatTTAAACT aagataatat atgcacagt atgtgcagga acaacttcct 1620  
 agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680  
 cttttaaaat aaaacagaga ggatgcata gaggctgata gaagacataa ctgaatgttc 1740  
 aatgtttgtt gggTTTtaag tcattcattt ccaaatttattt ttttttttcc ttttgggaa 1800  
 aggaaaggaa aaattataat cactaatctt gtttctttt aaattgtttg taacttggat 1860  
 gctgccgcta ctgaatgtt acaaattgct tgccctgctaa agtaaatgtat taaattgaca 1920  
 ttttcttact aaaaaaaaaaaaaaaa 1947

&lt;210&gt; 185

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

Met	Ala	Tyr	Met	Leu	Lys	Lys	Leu	Leu	Ile	Ser	Tyr	Ile	Ser	Ile	Ile
1				5				10					15		

Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
					20			25					30		

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
					35			40				45			

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
					50			55				60			

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
					65			70			75			80	

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
					85				90				95		

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
					100			105				110			

Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
					115			120				125			

Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
					130			135				140			

Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
					145			150			155		160		

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
					165			170				175			

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
					180			185				190			

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
                  195                     200                 205  
  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
                  210                     215                 220  
  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
                  225                     230                 235                 240  
  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
                  245                     250                 255  
  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
                  260                     265                 270  
  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
                  275                     280                 285  
  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
                  290                     295                 300  
  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
                  305                     310                 315                 320  
  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
                  325                     330                 335  
  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
                  340                     345                 350  
  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
                  355                     360                 365  
  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
                  370                     375                 380  
  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
                  385                     390                 395                 400  
  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
                  405                     410                 415  
  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
                  420                     425                 430  
  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
                  435                     440                 445  
  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
                  450                     455                 460  
  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465

470

475

480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro  
485 490 495

Phe Ala Asn Gly Ile  
500

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<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 186  
cctccctcta ttacccatqt c

21

<210> 187  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 187  
gaccaacttt ctctggagt gagg

24

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<210> 188
<211> 47
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 188  
gtcactttat ttcttctaaca acaaqctcgta atccttacca qtggcaq

47

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<210> 189  
<211> 2917  
<212> DNA  
<213> Homo sapiens
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<400> 189  
cccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaactg 60  
actttttta ttctttttt tccatcttg ggcagcttg ggatcctagg ccgcctggg 120  
aagacatttq tttttacac acataaqgat ctgtgtttqaq ggtttcttct tcctccccgtq 180
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acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
gcacttatct gcctaggatc atcgaagtct tttgacctcc atacagtat tatgcctgtc 300  
atcgctggg gtatcctggc ggccttgctc ctgctgatag ttgtctgtct ctgtctttac 360  
ttcaaaaatac aacaacgcgct aaaagctgca aaggAACCTG aagctgtggc tgaaaaaat 420  
cacaaccagg acaagggtgtg gtgggccaag aacagccagg cccaaaccat tgccacggag 480  
tcttgtctg ccctgcagtg ctgtgaagga tatagaatgt gtgcagatct tgattccctg 540  
ccacccctgt gttgcgacat aaatgaggc ctcgtgatca ggaaaggctc ccttctcaaa 600  
gcagagccct gaagacttca atgatgtcaa tgaggccacc tggttgat gtgcaggcac 660  
agaagaaaagg cacagctccc catcagttc atggaaaata actcagtgcc tgctggAAC 720  
cagctgtgg agatccctac agagagctt cactggggc aacccttcca ggaaggagtt 780  
ggggagagag aaccctcaact gtggggatg ctgataaaacc agtcacacag ctgtcttatt 840  
ctcacacaaa tctaccctt ggcgtggctgg aactgacgtt tccctggagg tgccagaaaa 900  
gctgatgtaa cacagagcct ataaaagctg tcggccctta aggctgccc ggccttgcc 960  
aaaatggagc ttgttaagaag gctcatgcca ttgaccctct taattctctc ctgtttggcg 1020  
gagctgacaa tggcgaggc tgaaggaat gcaagctgca cagtcagtct aggggggtgcc 1080  
aatatggcag agacccacaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140  
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gatccagatg gaagctgtga aagtggaaac attaaagtct ttgacgaaac ctccagcaat 1260  
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tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtctt 1380  
gtcttctact acttcttctc tcctaacatc tctattccaa actgtggcg ttacctggat 1440  
accttggaaag gatccctcac cagccccaa taccggaaagc cgccatctga gctggcttat 1500  
tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560  
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accactctg gcctgattgg acaagctgtt ggcgtgtga ctcccccctt cgaatcgatca 1680  
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<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

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 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
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 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
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 Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
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Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
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Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
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Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
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Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565	570	575
Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe 580	585	590
Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr 595	600	605
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<212> DNA		
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tctctatcc aaactgtggc g		21
<210> 192		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 192		
tttgatgacg attcgaagg tt		22
<210> 193		
<211> 47		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 193		
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<210> 194		
<211> 2362		
<212> DNA		
<213> Homo sapiens		
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&lt;210&gt; 195

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

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Leu	Leu	Leu	Leu	Leu	Pro	Pro	Pro	Pro	Cys	Pro	Ala	His	Ser	Ala	Thr
					20				25				30		

Arg	Phe	Asp	Pro	Thr	Trp	Glu	Ser	Leu	Asp	Ala	Arg	Gln	Leu	Pro	Ala	
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Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
 450 455 460

Asn Val Ile  
 465

<210> 196  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196  
 tggtttgacc aggc当地 gttt cggt 23

<210> 197  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197  
 ggattcatcc tcaaggaaga gctttt 24

<210> 198

<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 198  
aacttgcagc atcagccact ctgc 24

<210> 199  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 199  
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<210> 200  
<211> 2372  
<212> DNA  
<213> Homo sapiens

<400> 200  
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atacctaaga	agtacattgt	tacctctata	tacccaaagca	cattttaaaa	gtgcattaa	2280
caaatgtatc	actagccctc	cttttccaa	caagaaggga	ctgagagatg	cagaaatatt	2340
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<210> 201

<211> 322

<212> PBT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
 130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
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 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
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 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
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<210> 202  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 202  
 gagctttcca tccaggtgtc atgc 24  
  
 <210> 203  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 203
      gtcagtgaca gtacctactc gg                                22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 204
      tggagcagga ggagtagtag tagg                                24

<210> 205
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 205
      aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt    50

<210> 206
<211> 1620
<212> DNA
<213> Homo sapiens

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<221> modified_base
<222> (973)
<223> a, t, c or g

<220>
<221> modified_base
<222> (977)
<223> a, t, c or g

<220>
<221> modified_base
<222> (996)
<223> a, t, c or g

<220>
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&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

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&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1

5

10

15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20

25

30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35

40

45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50

55

60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65

70

75

80



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<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 209
tggagacaat atccctgagg                                20

<210> 210
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 210
aacagttggc cacagcatgg cagg                                24

<210> 211
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 211
ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag      50

<210> 212
<211> 1985
<212> DNA
<213> Homo sapiens

<400> 212
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<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr

1

5

10

15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
                  35                        40                        45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
           100                 105                 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr		
130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu		
145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg		
165	170	175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala		
180	185	190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly		
195	200	205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr		
210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro		
225	230	235
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp		
245	250	255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu		
260	265	270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu		
275	280	285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys		
290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser		
305	310	315
Val Arg Tyr Pro Val Val His Pro Asn Cys Gly Pro Pro Glu		
325	330	335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr		
340	345	350
Gly Val Tyr Cys Tyr Arg Gln His		
355	360	
<210> 214		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214

tgc~~t~~tcgct~~a~~ ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215

ttcc~~c~~tttg~~t~~ ggttggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216

agg~~g~~ctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217

agcc~~g~~atgag gaaatg~~c~~

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218

tgtccaaagt acacacacacct gagg

24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgcgcctt ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 cggaacttc cagtacgacc atgagggttt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccg tctggggcggt atcgtggacc gcatggaccg 300  
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 gcagcagcgg cacatacggg actcggtgag cgccgcctgg gacacgtacg acacggaccg 420  
 cgacggcggt gtgggttggg aggagctgctg caacgcacc tatggccact acgcgcgg 480  
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 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

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Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly			
20	25	30	
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
35	40	45	
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
50	55	60	
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
65	70	75	80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
85	90	95	
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
100	105	110	
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
115	120	125	
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
130	135	140	
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
145	150	155	160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
165	170	175	
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
180	185	190	
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
195	200	205	
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
210	215	220	
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala			
225	230	235	240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
245	250	255	
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
260	265	270	
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
275	280	285	

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290                            295                            300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305                            310                            315                            320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 225  
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt 44  
  
 <210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 226  
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&lt;210&gt; 227

<211> 550  
<212> PRT  
<213> Homo sapiens

<400> 227

Met	Ser	Ala	Ala	Trp	Ile	Pro	Ala	Leu	Gly	Leu	Gly	Val	Cys	Leu	Leu
1					5				10				15		

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile

20						25				30					
----	--	--	--	--	--	----	--	--	--	----	--	--	--	--	--

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val

35						40				45					
----	--	--	--	--	--	----	--	--	--	----	--	--	--	--	--

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn

50					55				60					
----	--	--	--	--	----	--	--	--	----	--	--	--	--	--

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg

65				70			75			80				
----	--	--	--	----	--	--	----	--	--	----	--	--	--	--

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro

85				90			95							
----	--	--	--	----	--	--	----	--	--	--	--	--	--	--

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln

100				105			110							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser

115				120			125							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro

130				135			140							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Thr Gly Lys Arg Leu Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys

145				150			155			160				
-----	--	--	--	-----	--	--	-----	--	--	-----	--	--	--	--

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile

165				170			175							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala

180				185			190							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln

195				200			205							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser

210				215			220							
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly

225				230			235			240				
-----	--	--	--	-----	--	--	-----	--	--	-----	--	--	--	--

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe

245				250			255							
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Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
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Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
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Phe Leu Glu Ser Gln Gln		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 233  
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<400> 233  
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<210> 234  
<211> 45  
<212> DNA  
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<210> 235  
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<212> DNA  
<213> Homo sapiens

<400> 235  
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gtcgggggcg cggctcgaaa cgcagacgg agatgcagcg gcttggggcc accctgtgt 180  
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aagagatggaa ggcagaagaa gctgtgtcta aagcatcatc agaagtgaac ctggcaaact 420  
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atgtgcaccc agaaaattcac aagataacca acaaccagac tggacaaatg gtctttcag 540  
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<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
                  35                 40                 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
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Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
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<210> 242
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<400> 242
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<210> 243
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<210> 244
<211> 3679
<212> DNA
<213> Homo Sapien

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<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu  
50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu  
65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly  
80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe  
95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu  
110 115 120

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser  
 155 160 165  
 Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile  
 170 175 180  
 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met  
 185 190 195  
 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg  
 200 205 210  
 Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu  
 215 220 225  
 Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu  
 230 235 240  
 Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg  
 245 250 255  
 Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys  
 260 265 270  
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 275 280 285  
 His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser  
 290 295 300  
 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu  
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 Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala  
 320 325 330  
 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn  
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 350 355 360  
 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys  
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 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile  
 380 385 390  
 Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg  
 395 400 405  
 Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys

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Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
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Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
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Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
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Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
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Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
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Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
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Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
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Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr		
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Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
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Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
605	610	615
Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
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                   695                      700                  705  
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<210> 246  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 246  
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<210> 247  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 247  
 aaacttgcg atggagacca gctc 24

<210> 248  
 <211> 45  
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<220>  
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<210> 249  
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 <212> DNA  
 <213> Homo Sapien

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&lt;210&gt; 250

<211> 546  
 <212> PRT  
 <213> Homo Sapien

&lt;400&gt; 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1					5					10					15

  

Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
					20				25					30

  

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
				35				40						45

  

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
				50				55						60

  

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
				65				70						75

  

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
				80				85						90

  

Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His  
 365 370 375  
 Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile  
 380 385 390  
 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
 395 400 405  
 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
 410 415 420  
 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
 425 430 435  
 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
 440 445 450  
 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
 455 460 465  
 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
 470 475 480  
 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
 485 490 495  
 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly  
 500 505 510  
 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp  
 515 520 525  
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 Ala Asp Lys Glu Gln Ala  
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 <211> 24

<212> DNA  
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<400> 252  
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<210> 253  
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<212> DNA  
<213> Homo Sapien

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tgggattatg tgacggtccg caaggatgcc tacatgttctt ggtggctcta 200  
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&lt;210&gt; 255

&lt;211&gt; 452

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 255

Met	Glu	LLeu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1										10			15	

Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
												20	25	30

Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
												35	40	45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn  
                   50                      55                      60

Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln  
                   65                      70                      75

Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu  
                   80                      85                      90

Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp  
                   95                      100                    105

Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr  
                   110                      115                    120

Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu  
                   125                      130                    135

Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe  
                   140                      145                    150

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser  
                   155                      160                    165

Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu  
                   170                      175                    180

Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly  
                   185                      190                    195

Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu  
                   200                      205                    210

Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys  
                   215                      220                    225

Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala  
                   230                      235                    240

Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys  
                   245                      250                    255

Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr  
                   260                      265                    270

Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser  
                   275                      280                    285

Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His  
                   290                      295                    300

Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450
Gln Glu		
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&lt;210&gt; 257

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Ala	Arg
1					5				10			15	

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
					20				25			30		

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
					35				40			45		

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
					50				55			60		

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
					65				70			75		

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
						80			85			90		

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
 95 100 105  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
 275 280 285  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
 290 295 300  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
 305 310

&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

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159

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<210> 259  
 <211> 556  
 <212> PRT  
 <213> Homo Sapien

<400> 259  
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35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly  
 290 295 300  
 Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser  
 305 310 315  
 Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp  
 320 325 330  
 Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met  
 335 340 345  
 Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp  
 350 355 360  
 Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg  
 365 370 375  
 Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly  
 380 385 390  
 Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp  
 395 400 405  
 Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser  
 410 415 420  
 Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His  
 425 430 435  
 Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro  
 440 445 450  
 Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg  
 455 460 465  
 Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val  
 470 475 480  
 Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser  
 485 490 495  
 Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln  
 500 505 510  
 His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser  
 515 520 525  
 Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro  
 530 535 540  
 Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu  
 545 550 555

## Cys

<210> 260  
 <211> 1638  
 <212> DNA  
 <213> Homo Sapien

<400> 260  
 gccgcgcgct ctctccccgc gcccacacct gtctgagcgg cgca... 50  
 cgcggcccgg gcgggatgtct cggcgccggaa cagtgtcg... catggcagg... 100  
 attccagg... tcctcttc... tctttt... ctgtctgt... ctgttgg... 150  
 agtgagcc... tacagtgc... cctggaaacc cacttgg... gcataacc... 200  
 tccctgtcg... cttgcccc... tctacc... attagcc... gccagact... 250  
 ggagcc... ccaaatt... agtatctt... tcatgtgg... cccagtgt... 300  
 taagg... ccactgccc... cttacga... gcca... tatctgt... 350  
 atgaaaacg... ctatgcca... ggcagg... caga... ggtggg... 400  
 tacatc... gcagt... agatgg... caacacc... actcagg... 450  
 ttca... tctc... agcgg... ttatgg... gacagc... 500  
 tcagcatt... tgg... aagg... ttct... actacc... ctca... 550  
 gtgaagtt... ccacgg... cacc... ctgg... aga... 600  
 cctcacag... gccc... tacacg... aaaa... gtgaa... 650  
 cccagaag... tcgag... ttct... ccaag... agatgg... 700  
 cgaggg... acgact... ttcag... cccg... tgaa... 750  
 gtggatcc... gtgaa... cccat... caagg... atcaagg... 800  
 atgccaat... catcg... gattat... atgc... ggaact... 850  
 aagccccaca... agagaa... tatga... ggggtg... ctc... 900  
 gcagctg... gggggc... ttcactt... tgg... aatgacc... 950  
 caggcaattt... ggtgtat... ttctgt... tcaa... gac... 1000  
 ttgtctacc... agcaat... tgccc... gggcc... ggtct... 1050  
 ctatgtgagg... atgtg... gac... gaag... cgg... 1100

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gatttcaacg tggctgtcag aatcactcct ctcaaataatg cccagattt 1200  
 ctattggatt aaaggaaaact acctggattt tagggagggg tgacacagtg 1250  
 ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300  
 ccaaattgtt ttttgcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
 tgtgtgtaaag gtgtcttata atctttacc tatttcttac aattgcaaga 1400  
 tgactggctt tactatttga aaactggttt gtgtatcata tcatastatca 1450  
 tttaaggagt ttgaaggcat acttttgcatt agaaataaaaa aaaatactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgttttg 1550  
 caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaaaaaaaaa 1638

&lt;210&gt; 261

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
1						5				10				15

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
						20				25				30

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
						35				40				45

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
						50			55				60	

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
						65			70				75	

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
						80			85				90	

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
							95			100				105

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
							110		115				120	

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser  
 125 130 135  
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe  
 140 145 150  
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val  
 155 160 165  
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly  
 170 175 180  
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu  
 185 190 195  
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr  
 200 205 210  
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys  
 215 220 225  
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp  
 230 235 240  
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro  
 245 250 255  
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys  
 260 265 270  
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp  
 275 280 285  
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu  
 290 295 300  
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala  
 305 310 315  
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln  
 320 325 330  
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp  
 335 340 345  
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg  
 350 355 360  
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly  
 365 370 375  
 Asn Tyr Leu Asp Cys Arg Glu Gly  
 380

<210> 262  
<211> 1378  
<212> DNA  
<213> Homo Sapien

<400> 262  
gcatgcgcct gggctctcg agcctgctgc ctgctcccc gccccaccag 50  
ccatggtggt ttctggagcg ccccccagccc tgggtgggg ctgtctcgcc 100  
accttcacctt ccctgctgct gctggcgctcg acagccatcc tcaatgcggc 150  
caggataacctt gttcccccag cctgtggaa gccccagcag ctgaaccggg 200  
ttgtggcgcc cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300  
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350  
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
cggtcccaaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450  
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctgt otcgagcgct 500  
ccatacagtt ctcagagcgg gtcctgccc tctgcctacc tgatgcctct 550  
atccacactcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600  
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
ttcctatcat cgactcgaa gtctgcagcc atctgtactg gccccggagca 700  
ggacagggac ccatcaactga ggacatgctg tgtccggct acttggaggg 750  
ggagcggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850  
gccgagcgca acaggccccgg ggtctacatc agcctctctg cgccaccgctc 900  
ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
gggggtggggc cctcaggcgca ccgagccagg gctctggggc cgccgcgcgc 1000  
tccttagggcg cagcgggacg cggggctcgat atctgaaagg cggccagatc 1050  
cacatctgga tctggatctg cggcggcctc gggcggttcc ccccgccgta 1100  
aataggctca tctacactcta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200  
 catcaggccc cgcccaacgg cctcatgtcc cgcgcac 1250  
 cccgcccccg ggccccagcg ctttgcata tataaatgtt aatgatttt 1300  
 ataggtattt gtaaccctgc ccacatatct tatatttcc tccaatttc 1350  
 ataaattatt tattctccaa aaaaaaaaa 1378

&lt;210&gt; 263

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
1					5					10				15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
		20								25				30
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35						40				45
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50				55						60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65						70				75
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
				80					85					90
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
				95				100						105
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
				110					115					120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
				125				130						135
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
				140					145					150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
				155					160					165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
				170					175					180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu  
                  185                     190                     195  
 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His  
                  200                     205                     210  
 Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met  
                  215                     220                     225  
 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly  
                  230                     235                     240  
 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu  
                  245                     250                     255  
 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn  
                  260                     265                     270  
 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val  
                  275                     280                     285  
 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly  
                  290                     295                     300  
 Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala  
                  305                     310                     315  
 Arg Ser  
 <210> 264  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
 <400> 264  
 gtccgcaagg atgcctacat gttc 24  
 <210> 265  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
 <400> 265  
 gcagaggtgt ctaaggttg 19  
 <210> 266  
 <211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 266  
agctctagac caatgccagc ttcc 24

<210> 267  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 267  
gcccccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 268  
ggggattca ccctatgaca ttgcc 25

<210> 269  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 269  
gaatgccttg caagcatcaa ctgg 24

<210> 270  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 270  
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatggcac tccaaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccgaggc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
gggcaggat tccagggttc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcagggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgatt gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280  
ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281  
cgtctcgagc gtcataaca gttcccttgc ccca 34

<210> 282  
<211> 61  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282  
tggaggggga gcgggatgct tgtctggcg actccggggg cccccatg 50  
tgccaggtgg a 61

<210> 283  
<211> 119  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283  
ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50  
gcagccatct gtactggcg ggagcaggac agggacccat cactgaggac 100  
atgctgtgtg ccggctact 119

<210> 284  
<211> 1875  
<212> DNA  
<213> Homo Sapien

<400> 284  
gacggctggc caccatgcac ggctcctgca gtttcctgat gtttctgctg 50  
ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggtagact gcacaacctc taccgggccc 150  
aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt gggccacaa 250  
caaggagcgc gggcgccgag gcgagaatct gttcgccatc acagacgagg 300  
gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
tacaacctca ggcgcgcccac ctgcagccca ggccagatgt gcggccacta 400  
cacgcaggtg gtatggcca agacagagag gatcggctgt gttcccact 450  
tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500  
tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550  
ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600  
tctgtgaacc catcggaaagc ccggaaagatg ctcaggattt gccttacctg 650  
gtaactgagg ccccatcatt ccggcgact gaagcatcag actctaggaa 700  
aatgggtact cttttttccc tagcaacggg gattccggct ttcttgtaa 750  
cagaggtctc aggctccctg gcaaccaagg ctctgcctgc tgtggaaacc 800  
caggccccaa cttcccttagc aacgaaagac ccgcctcca tggcaacaga 850  
ggctccaccc tgcgttaacaa ctgaggtccc ttccattttgcagctcaca 900  
gcctgcctc cttggatgag gagccagttt cttcccccata atcgacccat 950  
ttccctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000  
ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050  
caagggaaact cttcccccattt gcccaggagg aggctgagggc tgaggctgag 1100  
ttgcctccctt ccagtgaggt cttggcctca gttttccag cccaggacaa 1150  
gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200  
agtccctgcc caattttttttt aatacctctg ccaccgctaa tgccacgggt 1250  
gggcgtgccc tggctctgca gtcgtccttgc ccaggtgcag agggccctga 1300  
caagccttagc gttgtgtcag ggctgaactc gggccctggc catgtgtggg 1350  
gcctctccat gggactactg ctccctgcctc ctctgggtt ggctggaatc 1400

ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450  
 catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500  
 gccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
 atcctggagg cacaaggcct ggctggctgc gagtcagga ggccgcctga 1600  
 ggactgcaca cggggccac acctctcctg cccctccctc ctgagtccctg 1650  
 ggggtggag gatttggagg agctcaactgc ctacctggcc tggggctgtc 1700  
 tgcccacaca gcatgtgcgc tctccctgag tgcctgtgt a gctggggatg 1750  
 gggattccta gggcagatg aaggacaagc cccactggag tggggttctt 1800  
 tgagtgggg aggcaaggac gagggaaagg aagtaactcc tgactctcca 1850  
 ataaaaaacct gtccaaacctg tgaaa 1875

&lt;210&gt; 285

&lt;211&gt; 463

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu
1														15
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
			20						25					30
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
				35					40					45
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
					50				55					60
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
				65					70					75
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Gly	Glu	Asn	Leu	Phe	
				80					85					90
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
				95					100					105
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
				110					115					120
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
				125					130					135

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu  
 140 145 150  
 Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr  
 155 160 165  
 Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly  
 170 175 180  
 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser  
 185 190 195  
 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro  
 200 205 210  
 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser  
 215 220 225  
 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile  
 230 235 240  
 Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys  
 245 250 255  
 Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr  
 260 265 270  
 Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr  
 275 280 285  
 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu  
 290 295 300  
 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile  
 305 310 315  
 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser  
 320 325 330  
 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly  
 335 340 345  
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Ala Glu Ala Glu  
 350 355 360  
 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro  
 365 370 375  
 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr  
 380 385 390  
 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser  
 395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
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 <212> PRT  
 <213> Homo Sapien

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20															25	30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
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 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
           50                        55                         60  
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
           65                        70                         75  
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
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 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
           95                        100                     105  
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
           110                        115                     120  
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
           125                        130                     135  
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
           140                        145                     150  
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn  
                                     155                        160                     165  
 Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala  
           170                        175                     180  
 Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met  
           185                        190                     195  
 Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu  
           200                        205                     210  
 Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly  
           215                        220                     225  
 Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn  
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 Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu  
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 Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn  
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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
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Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
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Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
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Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
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Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
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Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
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Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
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His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
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Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

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                   575                  580                  585  
  
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val  
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 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser  
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 Gly Gly Ser Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
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 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
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 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
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 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
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 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
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Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
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 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
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 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
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 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
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 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
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 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
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 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
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 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 920                        925                        930  
  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
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 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
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 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
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 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995                        1000                        1005  
  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
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 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
 1025                        1030                        1035  
  
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&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln	35	40	45
Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val	50	55	60
Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser	65	70	75
Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile	80	85	90
Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu	95	100	105
Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe	110	115	120
Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg	125	130	135
Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu	140	145	150
Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser			

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Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly		
170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly		
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg		
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp		
215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln		
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile		
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val		
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp		
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His		
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp		
305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys		
320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp		
335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro		
350	355	360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys		
365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn		
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val		
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp		
410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
                   425                  430                  435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
                   440                  445                  450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
                   455                  460                  465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
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&lt;210&gt; 293

&lt;211&gt; 4053

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 293

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Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
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Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		
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Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
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Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
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Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
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Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
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<220>  
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<400> 311  
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<210> 312  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 312  
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<210> 313  
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<212> DNA  
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<220>  
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<400> 313  
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<210> 314  
<211> 3003  
<212> DNA  
<213> Homo Sapien

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 <211> 509  
 <212> PRT  
 <213> Homo Sapien

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Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys		
35	40	45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys		
50	55	60

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys		
65	70	75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu		
80	85	90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met		
95	100	105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met		
110	115	120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met		
125	130	135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg		
140	145	150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg		
155	160	165

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 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys  
                  185                 190                 195  
  
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr  
                  200                 205                 210  
  
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys  
                  215                 220                 225  
  
 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys  
                  230                 235                 240  
  
 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr  
                  245                 250                 255  
  
 Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro  
                  260                 265                 270  
  
 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn  
                  275                 280                 285  
  
 Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro  
                  290                 295                 300  
  
 Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr  
                  305                 310                 315  
  
 Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro  
                  320                 325                 330  
  
 Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr  
                  335                 340                 345  
  
 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala  
                  350                 355                 360  
  
 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln  
                  365                 370                 375  
  
 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val  
                  380                 385                 390  
  
 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu  
                  395                 400                 405  
  
 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly  
                  410                 415                 420  
  
 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly		
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser		
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
500	505	

<210> 316  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 316  
gatggttcct gctcaagtgc cctg 24

<210> 317  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 317  
ttgcacttgt aggacccacg tacg 24

<210> 318  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 318  
ctgatggag gacctgtgta gatgttgcgt aatgtgctac aggaagagcc 50

<210> 319  
<211> 2110  
<212> DNA

<213> Homo Sapien

<400> 319

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caacaggtgc ttgctcgaaaa ctgaagggtga cagtgccatc acacactgtc 150  
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<210> 320  
 <211> 450  
 <212> PRT  
 <213> Homo Sapien

<400> 320  
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       20                  25                                 30  
 Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe  
       35                  40                                 45  
 His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg  
       50                  55                                 60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser  
                   65                     70                    75

Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro  
                   80                     85                    90

Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu  
                   95                     100                   105

Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu  
                   110                     115                   120

Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr  
                   125                     130                   135

Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr  
                   140                     145                   150

Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg  
                   155                     160                   165

Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser  
                   170                     175                   180

Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala  
                   185                     190                   195

Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg  
                   200                     205                   210

Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile  
                   215                     220                   225

Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu  
                   230                     235                   240

Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu  
                   245                     250                   255

Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp  
                   260                     265                   270

Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro  
                   275                     280                   285

Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp  
                   290                     295                   300

Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu  
                   305                     310                   315

Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

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335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Asp His Pro Glu		
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<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

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<210> 322

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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 322  
cactgacagg gttcctcacc cagg 24

<210> 323  
<211> 45  
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 20 25 30  
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 35 40 45  
 Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln  
 50 55 60  
 Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp  
 65 70 75  
 Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
 80 85 90  
 Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His  
 95 100 105  
 Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
 110 115 120  
 Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile  
 125 130 135  
 Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
 140 145 150  
 Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys  
 155 160 165  
 His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
 170 175 180  
 Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
 185 190 195  
 Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
 200 205 210  
 Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

215                    220                    225  
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu  
230                    235                    240  
Ala Asp Glu Glu Asp Val Ser Glu Glu Ala Glu Ser Lys Glu  
245                    250                    255  
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser  
260                    265                    270  
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser  
275                    280  
  
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 35 40 45  
 Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
 50 55 60  
 Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp  
 65 70 75  
 Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val  
 80 85 90  
 Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu  
 95 100 105  
 Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg  
 110 115 120  
 Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala  
 125 130 135  
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 140 145 150  
 Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser  
 155 160 165  
 Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly  
 170 175 180  
 Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln  
 185 190 195  
 Leu Asp Ala Gly Glu Glu Ala Thr Thr Lys Ser Gln Val Leu  
 200 205 210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg  
 215 220 225  
 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His  
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 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu  
 245 250 255  
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu  
 260 265 270  
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro  
 275 280 285  
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys  
 290 295 300  
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 305 310 315  
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu  
 320 325 330  
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met  
 335 340 345  
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 350 355 360  
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 365 370 375  
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp  
 380 385 390  
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile  
 395 400 405  
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn  
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 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg  
 425 430 435  
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala  
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 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr  
 455 460 465  
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr  
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Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
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Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
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<210> 338  
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<212> DNA  
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&lt;210&gt; 339

&lt;211&gt; 772

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 339

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Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
									35			40		45

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
						50			55			60		

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
									65			70		75

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
									80			85		90

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
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Val Leu Thr Ser Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val	
110	115	120
Asn Arg Thr Val Ala His His Phe Pro	Arg Leu Leu Tyr Phe Thr	
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala	Gly Met Gln Val Val Ser	
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu	Met Ser Glu Thr Leu Arg	
155	160	165
His Leu His Thr His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile	
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro	Arg Leu Ala Ala Leu	
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala	
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala	Arg Tyr Cys His Gly	
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg	
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro	
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp	Ser Leu Gly Val Gly	
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu	
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly	Ser Ser Ala Phe Leu	
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr	
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu	Glu Leu Glu Arg Ala Tyr	
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Ser Glu Ile Glu Gln Leu Gln Ala Gln	Ile Arg Asn Leu Thr Val	
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu	Ser Trp Pro Val Gly Leu	
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Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp  
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 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala  
                   380                  385                  390  
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp  
                   395                  400                  405  
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro  
                   410                  415                  420  
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg  
                   425                  430                  435  
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu  
                   440                  445                  450  
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg  
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 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met  
                   470                  475                  480  
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu  
                   485                  490                  495  
 Leu Val Ala Glu Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe  
                   500                  505                  510  
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu  
                   515                  520                  525  
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp  
                   530                  535                  540  
 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg  
                   545                  550                  555  
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala  
                   560                  565                  570  
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro  
                   575                  580                  585  
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly  
                   590                  595                  600  
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp  
                   605                  610                  615  
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu  
                   620                  625                  630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
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 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
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 Gln Glu Gln Ala Asn Ser Thr  
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 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

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 <212> PRT  
 <213> Homo Sapien

<400> 341

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Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	Leu	Gln	
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Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
					50				55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
					65				70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
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Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
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Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
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Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
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Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
					140				145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
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Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
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Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
					185				190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
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Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
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Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
					230				235					240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
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Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln  
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly  
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&lt;210&gt; 377

&lt;211&gt; 219

&lt;212&gt; PRT

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&lt;400&gt; 377

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Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
				35					40					45

Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
				50					55					60

Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser
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Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
					80				85					90

Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
					95				100					105

Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
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Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
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Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
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Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
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Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
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Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
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Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
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Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
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Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Ile	Gln	Asp	Glu	Gln	Thr
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Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
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Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
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Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
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Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val
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Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
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Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Gly
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Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
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Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly  
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Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly  
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